REMARKS

The Office has required restriction of Claims 1-8 into the following groups:

Group I: Claim 1, drawn to an oligonucleotide for detection of Salmonella toxin gene invA mRNA.

Group II: Claim 2, drawn to an oligonucleotide for detection of Salmonella toxin gene stn mRNA.

Group III: Claims 3 and 5-8, drawn to a process of amplifying Salmonella gene invA mRNA.

Group IV: Claims 4-8, drawn to a process of amplifying Salmonella gene stn mRNA.

Upon election of either Group I or Group II, the Examiner also required an election of a single nucleic acid for examination purposes. Upon election of either Group III or Group IV, the Examiner required an election of two nucleic acid sequences, as noted in the present Election/Restriction Requirement. The Examiner asserted that this requirement is not to be construed as a requirement for an election of species, since each compound is not a member of a single genus of invention, but constitutes an independent and patentably distinct invention.

Applicants elect, with traverse, the claims (Claims 3 and 5-8) of Group III for further prosecution. Applicants further elect, with traverse, the following sequences, SEQ ID NO: 4 and SEQ ID NO: 23.

Applicants submit that the Office has not made a proper restriction. Restriction is only proper if the claims of the restricted groups are either independent or patentably distinct. There also must be a serious burden on the Examiner if restriction is required. The burden of proof is on the Office to provide reasons and/or examples to support any conclusion in support of restriction (see MPEP § 803). Applicants respectfully submit that the Office has not demonstrated that it would be a serious burden to examine the entire application.

The Examiner has stated that the above requirement to select specific oligonucleotide sequences is not to be construed as a requirement for an election of species, asserting that the compounds (oligonucleotides) are not members of a single genus. Applicants respectfully traverse, based on the ground that within each claim, the recited oligonucleotide sequences do share the same genus properties in terms of structure and function. For example, in Claim 1,

those sequences (SEQ ID NOS: 1-12) that are capable of specifically binding Salmonella gene invA mRNA fall within a genus. Since these oligonucleotides bind to the same gene, they share structural and functional similarities, and therefore there is no serious burden to examine them together. Similarly, in Claim 2, those sequences (SEQ ID NOS.: 13-18) that are capable of specifically binding Salmonella gene stn mRNA fall within a genus, and are thus structurally and functionally similar. In addition, oligonucleotide sequences, SEQ ID NOS: 19-23 contain sequences homologous to portions of the Salmonella gene invA mRNA, and thus, fall within a genus, and oligonucleotide sequences, SEQ ID NOS: 24-27 contain sequences homologous to portions of the Salmonella gene stn mRNA sequence, and thus fall within a genus. Each group of these oligonucleotides also represents structurally and functionally similar species of the respective genus, and therefore there is no serious burden to examine them together. Thus, for at least these reasons, the requirement to elect specific oligonucleotide sequences, and in the present action, the election of SEQ ID NO: 4 and SEQ ID NO: 23, should be construed as an election of species. If the elected species are allowable over the prior art, the Examiner should conduct a search of the non-elected species.

Moreover, Applicants respectfully submit that if the invention is so narrowed, as to cover only one or two oligonucleotide sequences, Applicants cannot adequately claim the invention, which is to provide oligonucleotides capable of complementarily binding to intramolecular regions of the Salmonella toxin gene invA mRNA and the gene stn mRNA, and the related processes using these oligonucleotides, alone, or in combination with other respective oligonucleotides, having a sequence homologous to a portion of the Salmonella toxin gene invA mRNA or the gene stn mRNA. If the Examiner forces the election of one species at a time, Applicants cannot fully claim all the permutations of the present invention without filing numerous patent applications, which is an undue burden on the Applicants.

The Examiner required restriction among the recited oligonucleotide sequences in each claim. Applicants traverse for the following reasons. Each claim recites sufficiently few oligonucleotides, such that a search and examination of all the recited oligonucleotides, at one time, would not impose a serious burden on the Examiner. The oligonucleotides recited in Claims 1 and 2 are also classified in the same class, class 536, and thus, a search of the oligonucleotides in each claim would not impose a serious burden. Moreover, nucleotide sequences, SEQ ID NOS: 19-23 have the same initial 28 bases, and nucleotide sequences, SEQ ID NOS: 24-27 also have the same initial 28 bases, such that an examination of these particular groups of sequences would not place a serious burden on the Examiner. Therefore,

for at least these reasons, there is no serious burden to search and examine all the recited oligonucleotides in a claim, and thus in the present action, no undue burden to search and examine SEQ ID NOS: 1-12 and SEQ ID NOS: 19-23 at one time.

The Examiner required restriction among the product claims (Claims 1 and 2) and the process claims (Claims 3-8). Applicants respectfully traverse, based on the following reasons. Claims 1 and 2 are drawn to specific oligonucleotides. Claims 3-8 are drawn to processes that are characterized by the use of these oligonucleotides. In terms of the restriction of Claims 1 and 2, with the respective process claims, the Examiner has only made a general determination that the oligonucleotides in Claims 1 and 2 can be used in a materially different process, such as in a hybridization assay. Applicants submit that the Office has not demonstrated that a search of Claim 1 or Claim 2 with the respective process claims would impose a serious burden on the Office. Applicants note that hybridization is a general process for joining two complementary strands of nucleic acids. This process is generally used in amplification and detection processes of genes or oligonucleotide segments, and thus, cannot be considered a materially different process. Therefore, for at least the above reasons, it would not be a serious burden for the Examiner to examine the product and respective process claims together, and thus in the present action, to examine Claims 1, 3 and 5-8 together.

The Examiner required restriction among the claims, as divided between Groups I – IV, as noted in the Election/Restriction Requirement. Applicants traverse this for the following reasons. The oligonucleotides recited in these claims are involved in the detection and amplification of two genes which both derive from Salmonella. In addition, the detection and amplification of these genes involve similar method steps. Therefore, for at least these reasons, there is no serious burden to examine all claims at one time.

Accordingly, for at least the reasons presented above, Applicants submit that the Office has failed to meet the burden necessary, in order to sustain the requirement for restriction and election in the present application. Applicants respectfully request the withdrawal of the Restriction/Election Requirement.

Applicants respectfully submit that the present application is now in condition for examination on the merits, and early notice of such action is earnestly requested.

Respectfully submitted,

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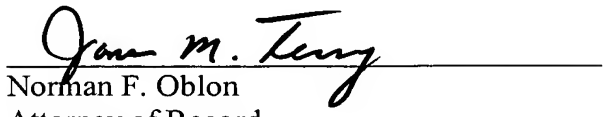

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